1/13

FIG. 1

```
         10                    30                       50
GTGAAGAACGAAAAAACCTTCTTTGAAGAGCTTTACGAGGCTTTAGAGGAAACCCACGAC
M K N E K T F F E E L Y E A L E E T H D
         70                    90                      110
AACACCGATGCCACTAGGGGGTCAGATAGGGGGTCAGAGGACTTCTTCTTGGCCACCGAC
N T D A T R G S D R G S E D F F L A T D
        130                   150                      170
CCCCCTCCAGATGGAGGTGCCGAAAATCGCCTCGCGAAGGGCTTTACATACCAAAAAGAG
P P P D G G A E N R L A K G F T Y Q K E
        190                   210                      230
GCACTTAGGATTGCTTTACCCGAGAAAGACCATGAGGCTTTCCTTTCCTCTGTTGGGGCC
A L R I A L P E K D H E A F L S S V G A
        250                   270                      290
CCCCCTATACCACCAGCTGAACCCCCCGTTGGGAATGTATGTCAAGCCGTCCAGGACGGG
P P I P P A E P P V G N V C Q A V Q D G
        310                   330                      350
CCTCAGAAGCTTCTGGAACTCCTCCAGGAGATTGCCCGCTCCACCATCCCCTACGGCAAC
P Q K L L E L L Q E I A R S T I P Y G N
        370                   390                      410
CGGGAGCTCTGGAGGAAGGTGGGGACGGTCGTCTTCATGGTCCCCCTGGAGATGTTGGCC
R E L W R K V G T V V F M V P L E M L A
        430                   450                      470
CTCAACCTGGGGGTCACCCGGCAGACCGTCCACGCCTGGAAGAAGGTCCTTGAGAAAAAG
L N L G V T R Q T V H A W K K V L E K K
        490                   510                      530
GGCCTGGTGGCCACCGACGTCCTTCACCAAACCGTCAACGGGGAGCGCCGGGCCATCGGC
G L V A T D V L H Q T V N G E R R A I G
        550                   570                      590
ACCCTTTGGGCCGTCCGGCTGAGGCCAGGGAAAGCCAGGCTCACCCTGGACGACTACATC
T L W A V R L R P G K A R L T L D D Y I
        610                   630                      650
TACCCCTGGAGGAACCTCGCCCTAGACATGGCCAACGGCGTGCTCTCCTTCAACTGGGTC
Y P W R N L A L D M A N G V L S F N W V
        670                   690                      710
AAGGCCTACCAGGACCACGGAATCCGCCCCACCCTGGACGTGCTGGTCCTCTGGGCTCAG
K A Y Q D H G I R P T L D V L V L W A Q
        730                   750                      770
GGGAAAAGGGTGATGCCCAACACCAAGACCGTGGCCGTTGACCTGGGCCTCATCCTGGTC
G K R V M P N T K T V A V D L G L I L V
        790                   810                      830
CTCCCCGAGGTGGAGCGTTCCAAACTCCCGGCCCTTATCACCCTCATTGCTACGTACATT
L P E V E R S K L P A L I T L I A T Y I
        850                   870                      890
GCCGATCTCCTAGATGACCGTCGTTCAAGACGTTTCTATGCAGGCTTGCTGTGGGCTGTG
A D L L D D R R S R R F Y A G L L W A V
        910                   930                      950
GCCAGGGGTGAACTCCCCGCGCAATATCTATTTGCCGTCCTAATGCGGGTTATCCGAGAT
A R G E L P A Q Y L F A V L M R V I R D
        970                   990                     1010
TACACGGATGGCCATCTGACACGACCGGGAGCGTACCTAGTGAAGACCCTCAAGGAGGCC
Y T D G H L T R P G A Y L V K T L K E A

TCCTGA
S *
```

2/13

FIG. 2

```
    1   CTATAACGGCCTTTTTAGGAGGGGGGGATTGCCAGCCGCTGGGCTGACGGTTATTTTGGACC

   61   CATAAAAAGGCGAAACCGAGGCGGTTGCCCCGGATCACCCCCAAGACCTAGGGTAACGCC

  121   TCGGGCTCCAGATGACAAGGAGGTCCGAGGGTGAAGAACGAAAAAACCTTCTTTGAAGAG
                                       M  K  N  E  K  T  F  F...(RepT)
```

BEST AVAILABLE COPY

3/13

FIG. 3A

```
   1 tctagaaggt cagggtggac aaggaaaaca ccatagcccc tgccaagaag atggacgagt
  61 tggtgtccgg aaaagtggcc atccggggcg ctcttgacaa ctatttttcca gcggtggcca
 121 ccggcattgg ccacgaggta cgagcttgtg gagtagacgg ccacaaaggg gtcgtcctca
 181 aacttctttt ctagtgccgc ttggacgaag gggaggaaga ggaaaggctt catggcctca
 241 cctccttccc ctcctccttg gcggccttag cggcgtaaaa ctctgagacg gcctgaagtt
 301 tagggatttc gctttcgggg ataagaatcc ggcggctcag gggatgccgg atggccctta
 361 tcctgccgtc ccttatgtac tcgtaaatgg tggccttggg tactttaaac cgttctgaaa
 421 cttctctaac agagagcaca aaacctctaa aaacctatca atcccaccga ttccagtata
 481 ccataaatgg cacaaagttt tgagaaggtg gtcaaacaaa aaggctttct cggtcaggtt
 541 atggtgaggt gggggcggtc aaaggccgac ttaagtttgg taaagccggg aggaagcaaa
 601 ccggggtgtt accatgcaac agatggccga gtggaacgtg tggacacaga gaagcgttga
 661 gcttctggag aagggggtatt tggataaact actgcaggtc tataaagggg aaagtggctc
 721 ttcgaggtca gtaccagagg aggtagagga aaaacttcgc gaggcctaca aggcatacga
 781 ggggaggcag gatagtccgg aggcagaaac gaaactcgtg gaagccgtgc taaatgccag
 841 aaaaaaggtc gagcggtccc ccttcaatca cccctacctg cctttggtct actacctggt
 901 ttcggaaaaa gcagaaaaag cgaacaaggc ccttgaggag gcattgcagg aggttgcctc
 961 aaagcaccca gaaaccatcc gcgtcctggc caaggaagcg caaagaagag gcgtagaagc
1021 cttgatccaa aggctcaagg agcctcccga aataaatcgg cagatagggc cgatgttcaa
1081 aaggtggtac aaagaagagc taaaggggaa aatagaagag aggcttccag gccctaccaa
1141 accaaagatt gtggtagtat cccctgaaaa aagtaaaccg gagcaagcac cccttattgc
1201 ggagagagaa gcgggcatca tcatatacac gggatcggat gaagctttga aagatgccgc
1261 caaggaaaac ctgggccttg gcgaggaagc agaactaggc accaagggcg tagatttcta
1321 cgtggtcatc cggcgtagcc ctgaagagac atggcaccta acaggagaag tgaagtttca
1381 atccgacttt ggcggaaacc aagacaacca gaaactagta gcaaaggctt ccataaggtt
1441 ggaccttgag aagaggcaca taggaatagt ggtggtggac ggaatgcctg tggtgagcaa
1501 gtttcgtggg tgggccggac tggggaaaga aacgatcgtt acatccgtac tcctccttcc
1561 agacctgata gcggagctct accaaaaggg tgaagaagcc ctgggcctct agaaggcgga
1621 cacaatctca aacttgtgct gtagcctggg gaaatcctct aacacccttc tagtgaaggc
1681 tttgaccgcc tcccaggagg catctatgcc gatggatcgc cgctttaaga ggggtgaggc
1741 tataagcgta gtaccggagc ctgcgaaggg atcgagcact aaatcccct cgttactccc
1801 tgtttggacg atgagcttga gcatgtccag attttttctcg gtggggtatc gcgggtacgg
1861 aggatccttg aactgccaaa cgtcctggag cttcttcccc ttcttcaggc gatcccgagc
1921 gtaaactttc ttccgcggca ccccgttctt tgaccagaca ataagccctt gagcgtctag
1981 ctcgtcaagc ttctccgggg gatagcgcca atgccgtcca ggaggggggaa gtattcctcg
2041 ccaaggcctt ccggtagggc catccttggt ttctccagga gcatgcaggg gattggtggt
2101 gtaccgttcc ccgttctcgt ctacaaaggg gaaaagccta gcgatctcct cttccgaata
2161 ggggctagcc gattcgttcc aaacgtagtc ccgcgttttg gagtagacga ggatcatgtc
2221 cttttgcgat ccgaaggcct tacgggaaaa gttttttggga tttgaagcga tgcgggcgat
2281 atggttaacg aagtttcgcc ggcaaagac ctcatcaagg atgagcttca cctcgaaccc
2341 gtatttctcg tctatgtgaa cgaagatcag tcctgagtcc gccatcagct ccctgagaag
2401 tatcaagcgc tccctcagga actccacaaa ctgaggacca tcgagggtgt catcgtagcc
2461 caactgaccg tttttgggct ggctgacggt agcaacgcga tctgtttcat cgccgccaac
2521 gagaaactgc tggccggttc cataaggcgg gtcaatatag accaactgga ccttccccgc
2581 atacccacca ggctcccgga gcatccaccg gagaacctga ccgtttttccc ccaaaaagta
2641 ggtgccaata ggatcaatct caaaaagggg ggcatttccc cctaggaaga ggagggtttc
2701 ttttcgcaaa acaagttgtg gggtgggctg atcaagaatc tcctctcat cgcgttttcc
2761 ggggtagacc aacctaaagg gcgaaggttc cgaggttttc gaggctttca aggggcttt
2821 tcgggtcaaa ccagggtagc tacggctcat tcttccctcc ccacagcgct cttaagcagg
2881 acctcatcac ccacaaccct cacgcactcc aaccaaggaa tccgccaaag gcggcctacc
2941 ttttgagccc gtatcttccc ctgacgtata gaccttcgga tcgtctcagg gtgcacccga
3001 aggatgtctg caagctcctc gggggtcagg tacacgggct tcatcctcat gacacaacct
3061 tacccacag aggacaacac atgcaactat gggcaaagta gacaacgaga ccaaaagctt
3121 gggccactct ctcaggaggc ctccttgagg gtcttcacta ggtacgctcc cggtcgtgtc
3181 agatggccat ccgtgtaatc tcggataacc cgcattagga cggcaaatag atattgcgcg
3241 gggagttcac ccctggccac agcccacagc aagcctgcat agaaacgtct tgaacgacgg
3301 tcatctagga gatcggcaat gtacgtagca atgagggtga taagggccgg gagtttggaa
```

4/13

FIG. 3B

```
3361 cgctccacct cggggaggac caggatgagg cccaggtcaa cggccacggt cttggtgttg
3421 ggcatcaccc tttttcccctg agcccagagg accagcacgt ccagggtggg gcggattccg
3481 tggtcctggt aggccttgac ccagttgaag gagagcacgc cgttggccat gtctagggcg
3541 aggttcctcc aggggtagat gtagtcgtcc agggtgagcc tggctttccc tggcctcagc
3601 cggacggccc aaagggtgcc gatggcccgg cgctccccgt tgacggtttg gtgaaggacg
3661 tcggtggcca ccaggccctt tttctcaagg accttcttcc aggcgtggac ggtctgccgg
3721 gtgacccca ggttgagggc caacatctcc aggggggacca tgaagacgac cgtccccacc
3781 ttcctccaga gctcccggtt gccgtagggg atggtggagc gggcaatctc ctggaggagt
3841 tccagaagct tctgaggccc gtcctggacg gcttgacata cattcccaac gggggttca
3901 gctggtggta tagggggggc cccaacagag gaaaggaaag cctcatggtc tttctcgggt
3961 aaagcaatcc taagtgcctc tttttggtat gtaaagccct tcgcgaggcg attttcggca
4021 cctccatctg gagggggtc ggtggccaag aagaagtcct ctgacccct atctgaccc
4081 ctagtggcat cggtgttgtc gtgggtttcc tctaaagcct cgtaaagctc ttcaaagaag
4141 gtttttttcgt tcttcaccct cggacctcct tgtcatctgg agcccgaggc gttaccctag
4201 gtcttggggg tgatccgggg caaccgcctc ggtttcgcct ttttatgggt ccaaaataac
4261 cgtcagccca gcggctggca atccccctc ctaaaaggcc gttataggcc ctgctaggag
4321 gggggtagta cttcctacc ccctaggct tggagaggcc ttaggaggtc tcctagggcc
4381 tcgtgggggt gtaggggtaa cctcatggcc aggccggccg gctcgggact ctggaggagg
4441 cctccatagc ctactcgtgg tggaggtttg tgaaggggtt cactaatgca tacggctagc
4501 ctcgggatca cggccaaatg gtatgcaggt tttggtataa aaccctcagg tttgaggcta
4561 gtttatgtcg gttttatgca cctttgactc ggatcacggg cataaacacc agtttcctgc
4621 acgaaagaaa actttcgcga tctaagaggg ggaaagaggt gtagagggac ggccttcatg
4681 aaagttggcc tcttaggagg ccgttgtaga gggccgtctc gggttcaaat cctttccctc
4741 tctctccagg tttccgaggt tcgaggtctt ggtccaggtc ttgtaccaag tttttgacca
4801 aagtctattc tcggaatata ggggtatctt gtctatcttc cctacgggat atctctgtct
4861 gtgtgaactt gatcccatcc caatacatat ctcaatctcc taatctcctc ttctctccag
4921 atccctaatc tcttcttcta cctctttctc ctcccaatta agaatggaga ggaaaaaccc
4981 cgaccagaac gagcttctcg gggtcagttt cggtaatctc gggacaggtt ttcatcgtct
5041 aggacgagga ttagggcatg aaaaatgggc tttgacaaaa tctttctaaa aaatactccc
5101 cgaggttggg gaagtgccct cggggagaag attttggca gttagatgt tatgctctat
5161 cacgggccgg aggcctccac gataagttgt cttggccaag taccgggcca ggtcgggggt
5221 gctcttcagc gtggtgatgg tactttcacg gaagttcaca agtcctttta gaggcttcag
5281 gtcggggata gtgctcaagt actcccaagc gttctcgggc ccgtggtcgg ggagaaggac
5341 aaaggggtcg ggcaaaagtt catctttgta cttaggacgg attactttag cacctgataa
5401 cttcagggcc gttaagaagg gcctcacctc ggagacgggt ggaaggagga cgtgggcgtg
5461 gaagaagacg aaccccgatt tttgggaagt ctccctccag tttgatgatg aacgttggga
5521 ggaagccggc caggatgtct ttcatcgcgc ctcgaacctc ggacacataa aaaactttcg
5581 tgtttgtcag ggcaagagtg ctatgtatga ggtaaccttc gggagtacaa agtgcctcaa
5641 gccgccttc ccaacgctcc aaaactctag ggtcaggtgg tttaggtttt ctgaaaaact
5701 ctagctttc agtggtcatt cctcacccct ctagcacgta ctctggaagg taaacctttg
5761 acacagccggc caagtctagc gtctcccagt ccagttggtc tgggacgcgt gagaaggggga
5821 ggggcttggt gtagaggacc agaagaccc
```

BEST AVAILABLE COPY

5/13

FIG. 4
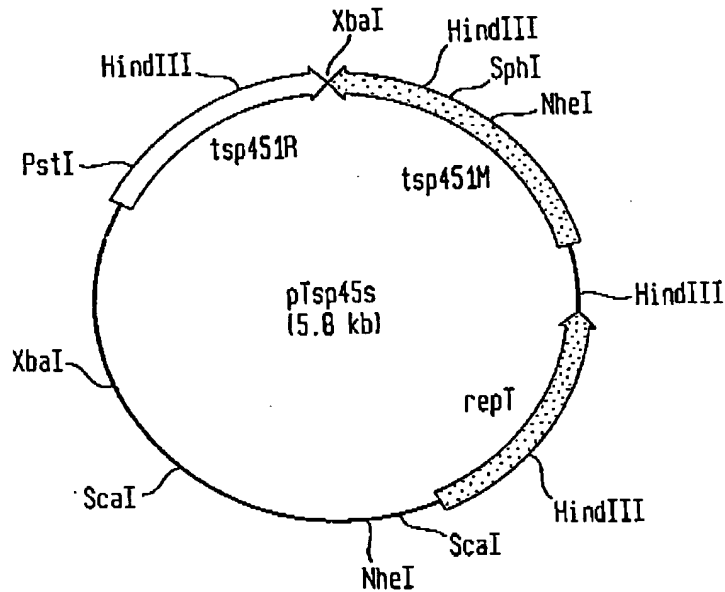
FIG. 5

```
  1  ATGATCGTGGCTGTCACCGGCTTCAAGGGGAGGGGTGGGGAAGACCACCACGGCGGTCCAC
     M  I  V  A  V  T  G  F  K  G  G  V  G  K  T  T  T  A  V  H
 61  CTGGCCTGCTTCCTGGCCGAGCGGGGGCCCCACCCTGCTGGTGGACGGGGACCCCAACCGC
     L  A  C  F  L  A  E  R  G  P  T  L  L  V  D  G  D  P  N  R
121  TCCGCCACGGGGTGGCACCGGAGGGGGAGGCCTCCCGGTGACCGTGGTGGACGAGCGGGTG
     S  A  T  G  W  H  R  R  G  G  L  P  V  T  V  V  D  E  R  V
181  GCGGCCCGGTACGCCCGGGAGCACGCCCACGTGGTCATAGACACCCAGGCCCGCCCCACG
     A  A  R  Y  A  R  E  H  A  H  V  V  I  D  T  Q  A  R  P  T
241  GAAGAGGACCTCCGGGCCCTCGCCAAGGGGGTGGACCTGCTGGTCCTGCCCACGTCCCCC
     E  E  D  L  R  A  L  A  K  G  V  D  L  L  V  L  P  T  S  P
301  GACGCCCTGGCCCTGGAGGCCCTCCTGGCCACCCTGGAAGCCCTGCGGGGGGGCGGAGGCC
     D  A  L  A  L  E  A  L  L  A  T  L  E  A  L  R  G  A  E  A
361  CGCTTCCGGGTCCTCCTGACCATGGTGCCCCCGCCCCCGAGCCGGGACGGGGAGGAGGCC
     R  F  R  V  L  L  T  M  V  P  P  P  P  S  R  D  G  E  E  A
421  CGGGCCCTCTTGGGGGCGGAGGGCGTTCCCCTCTTCACAGGCTGGGTGAGGCGGGCGGCA
     R  A  L  L  G  A  E  G  V  P  L  F  T  G  W  V  R  R  A  A
481  GCCTTCCCCAAGGCCGCCCTCCTGGGGGGTGCCTGTCTACCGGGTGCCCGACCCCAGGGCG
     A  F  P  K  A  A  L  L  G  V  P  V  Y  R  V  P  D  P  R  A
541  AGGCTGGCCTGGGGGGGACTACGCGCGGGTGGGGGAAGAGCTCCTGAAGGAGGTGGGGGGA
     R  L  A  W  G  D  Y  A  R  V  G  E  E  L  L  K  E  V  G  G
601  TGA 603
```

BEST AVAILABLE COPY

6/13

FIG. 6
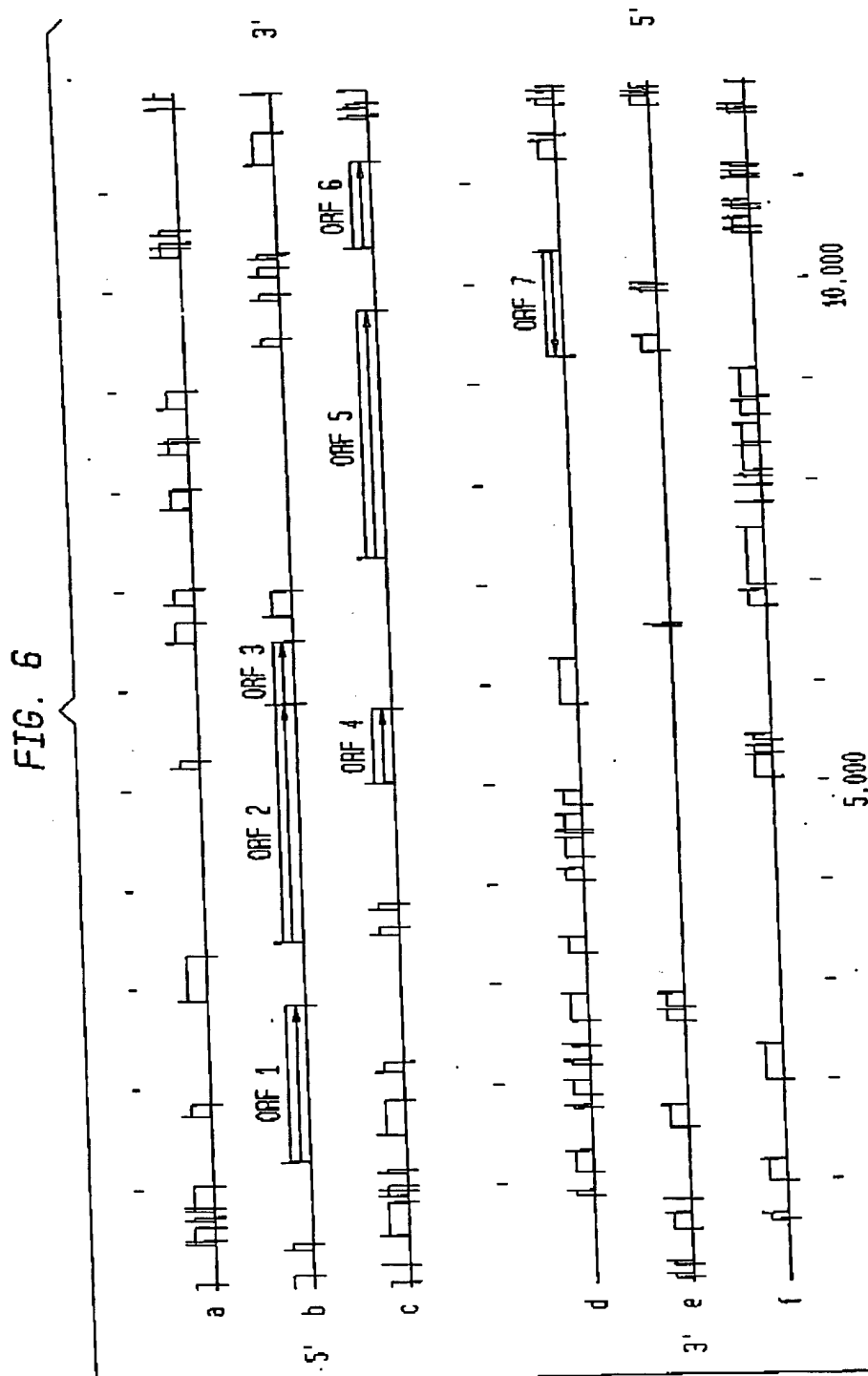
BEST AVAILABLE COPY

7/13

FIG: 7A

```
     CTTATACACACAAACTATACACGTCTCTATCGGGCTTTTCTTAGCGCCATGTAAAACACC
   1 --------+---------+---------+---------+---------+---------+  60
     CCTCCCATCTCCGGGTGTTTACAGCGGATACGGGAGGTTCAGCGGGAACTTTTCCCCTTG
  61 --------+---------+---------+---------+---------+---------+  120
     TTGAAACTTTGGGGTCTGAGGCTCAACAGCAGAACAGCTTAGGTTGACTCAACACAGCTC
 121 --------+---------+---------+---------+---------+---------+  180
     ATAAGTCCCTTCATTATCGCCTGAGTCAACCTATGAGTTAACCTTTTTTCAAGAAAAAGA
 181 --------+---------+---------+---------+---------+---------+  240
     GATAAGTGAGTTTTGTCCTCTAGCACGACTTTTTTCTTTGAGTCAACCTCTGTGCCGACC
 241 --------+---------+---------+---------+---------+---------+  300
     CCCCCGATTTTGAGTCAACCCCCCTTTGAGCCGAAACTTTGTTGGCACAGGGGTTGACTC
 301 --------+---------+---------+---------+---------+---------+  360
     AGGGGTTGACTCAACGCGAATGGCCTCTGGAAGGGCGTTGAGCCGACCCCTCCCTCGTGT
 361 --------+---------+---------+---------+---------+---------+  420
     GCCGACCCCCGCTCCACTATGAGCAGGGGGGAAAGTTACGGGAAAAGTTCCCCAAGTCCC
 421 --------+---------+---------+---------+---------+---------+  480
     CCTTGACAAAAGATGACAATCGAGTTAATGTCACAGCGATGCGTCACTCACCTCTGGCTG
 481 --------+---------+---------+---------+---------+---------+  540
     GGCTCACCCAGATGCGTGCGCGAACGTTTCAGAGCCTCCTTCGATTCCTGGCCAGGGAGG
 541 --------+---------+---------+---------+---------+---------+  600
     GGCGCTACCCCACTGGTGTAGAGCTCGCCAAGGTGCTGGGGCGCAGCCCGCACGCCACGT
 601 --------+---------+---------+---------+---------+---------+  660
     GGGCCATGCTCAGGGCTTTGACCCGTCATGGACTCGTGGAACGGCACGAGGGGGTCTATG
 661 --------+---------+---------+---------+---------+---------+  720
     TTCTGACCCCTGCGGGCGTAGAACTTGCCAGGACCCTGGGAACCACCGTGTGGCGTGGGG
 721 --------+---------+---------+---------+---------+---------+  780
     ATGAGGAGGTACAGACGGCGTTACAGCTGCTAGGAGTCGGTCATGCCGCCGAGGACAGGC
 781 --------+---------+---------+---------+---------+---------+  840
     GCTGAAGCTTTTGAGCCGGGGCCCTCACCCAAGGCCACCCCGGCTCCTCTCCCCTGGGAT
 841 --------+---------+---------+---------+---------+---------+  900
     CCCAAATGGATCCCTCAGCGCCATTATCCTCCTGGCGGTCCTATAGCGCAAGGAGGTAGT
 901 --------+---------+---------+---------+---------+---------+  960
     GGTGACGAAACACACAAATGTTTCACCCCACCTTTTGGATGCCGTAGAGGAGCTCGCTCG
 961 --------+---------+---------+---------+---------+---------+  1020
     CCAGATTGCTGAAACCGCTAACAAGGCTTATTCCAGCCATTTCAGGCAGATTGTCAAAGT
1021 --------+---------+---------+---------+---------+---------+  1080
     CCTGCCGCCTGAGGTTCCCGACCTCTACGCCTGGCTGGCCGCCCTGGATGACTCCGCCAT
1081 --------+---------+---------+---------+---------+---------+  1140
     CGAGGAGCTTGCCCAGCGCCTGAGGGAGGTCGAGGGAAGCCCCCGCCCCCATTTCACCGC
1141 --------+---------+---------+---------+---------+---------+  1200
     CGCCCTCAAAAAGGCCCTGGCCATCGCCCTACAGCGGCGGACCCTCGCCGAGATGCCCCC
1201 --------+---------+---------+---------+---------+---------+  1260
     CACGTTCGCCAACGCGCTCCGCTGGGCGATGGAACGGCAAGGGGTGAGCATCCGCAAGCT
1261 --------+---------+---------+---------+---------+---------+  1320
     TGCGAGAGAGGTAGGGGTCAGCAAAACCACTGTTAAAAAGTGGCGTGGAGGCCGCTTTGT
1321 --------+---------+---------+---------+---------+---------+  1380
     CCCTCGTTCACGGACCTACGTGAGGAGGTTGGAGGAGATCCTGGACCTCCCGGAAGGCGC
1381 --------+---------+---------+---------+---------+---------+  1440
     CCTTTCGGGACGACTACCCCGCTGGGGGTTGCCAAAAATATTGGAAGGTGTTGAGGGGAA
1441 --------+---------+---------+---------+---------+---------+  1500
     AGATGCCCCTTATCCCGGGTTCACGCGGACCTTCCTGCGCGTGGCCGCCCTGGCGCGCTA
1501 --------+---------+---------+---------+---------+---------+  1560
     CGGCCGCCCGTGGGATGATCTCTCTCCCGACGAACAGGAGGCCCTTCGGCGCGAGGACGA
1561 --------+---------+---------+---------+---------+---------+  1620
     AGACCGGTGGACCCGCCTCTCCAACCGCCAGAAGCGAGTGCGAAAGGCCAGTCAAAAACC
1621 --------+---------+---------+---------+---------+---------+  1680
     TTTTCGGCTTTCCTTTGACGAGTGGCCAACTGAGGCTCGCAAAGAATGGGAGGACTACGA
1681 --------+---------+---------+---------+---------+---------+  1740
     GCGCTATGCCTCATCGGCACCTGGGAGCATCGCGCGCGTGCAGGCGGCGCTTGCGGGCGC
1741 --------+---------+---------+---------+---------+---------+  1800
     ACCTCTCGCTCCCACGACCGTGCGGACGGAAACGCTCGAGCGTGAGCGGATACTTATAGA
```
1860

8/13

FIG. 7B

```
         ACTGTTCTACGGCTACTGTGTAAACGAACGGGGCCTCGACAGCAACGCGTTGAGCCTCGC
    1861 ---------+---------+---------+---------+---------+---------+ 1920
         CCTCCTCACAGACCTGGAGCTCGTCCAATCGTACCTGGAGTGGCGCGTGAATAGGTACAA
    1921 ---------+---------+---------+---------+---------+---------+ 1980
         GGACGAGGATTTACCCCCCGTTACTCGATCGGAATACATGTTTATCGCCCTGGTGAAAAA
    1981 ---------+---------+---------+---------+---------+---------+ 2040
         ACTCCACAGAGGTTATCTCCGCGCCCTTGGGCTTGGGGTAGACCCGGACGGGGTGAAAGA
    2041 ---------+---------+---------+---------+---------+---------+ 2100
         GCTGGAACGGAAACTGAAAATCGCCGGAATTGATGTCACGGACGGCTACCACGCGGTGGA
    2101 ---------+---------+---------+---------+---------+---------+ 2160
         GCCCCTCCTGGAAACTCACGAGCCCCTCCGCTGGGTGCTGGATGGCATCCGGCTCATGCT
    2161 ---------+---------+----.---+---------+---------+---------+ 2220
         CCGCGATGCGGCGGGGCGGGTAGGCAACCTGCTGACACCCCAAATCCCCACCGCCAAAAG
    2221 ---------+---------+---------+---------+---------+---------+ 2280
         CGAAGCGGGCGAAGCGTTCGCCCTCTACCGGGACGTCGTTCTGCTTTGGATGATGGTGGG
    2281 ---------+---------+---------+---------+---------+---------+ 2340
         CCACCCCCTCCGGGCGAAGCATTACTACGAAGCTCGCTTGGACATGAGCCAGTTCCAAGA
    2341 ---------+---------+---------+---------+---------+---------+ 2400
         CGGGGATTTCGCTCCCGGGCGGGGACACGTGGGGCGGGCCGGCGGAGGGTACTACCTGGC
    2401 ---------+---------+---------+---------+---------+---------+ 2460
         CTACCGCAAAGTGGAGTTCAAAAACGCCCGAGGCCAGGTCTTTCAGAGCCTCCAGGACCA
    2461 ---------+---------+---------+---------+---------+---------+ 2520
         CGATCTCGTCACGTTCCCCCTGGACGACCCCGAGCACCCTGTCCTGGTCCTGGACGTGAA
    2521 ---------+---------+---------+---------+---------+---------+ 2580
         CGGGATGCGGTACTCCCTCAACGAGCTCTTTCACGTCTACCTGCGCACGATCCTCTCCCG
    2581 ---------+---------+---------+---------+---------+---------+ 2640
         CCTGGCCCAGGCCTGGGCCGGACCGGTCCCCTCCTGCCCCTGTTTCCGGGTGCCGATACG
    2641 ---------+---------+---------+---------+---------+---------+ 2700
         AGGCTCAGACTTGCGCACATCGTTCGCAGGCGCGCCGCCTACGTGGCCGCCGTGCCCGGG
    2701 ---------+---------+---------+---------+---------+---------+ 2760
         GTACCCCAGAAACTTTTGCCCTTCGGCCCCCACTCCATCCGCCACGTGGTGGCCACGGAG
    2761 ---------+---------+---------+---------+---------+---------+ 2820
         GTCGTGAAGCGCACGGGCTCTTTTGAGGCCGCCGCCAACGTGCTCCTGGATAGCATAGAC
    2821 ---------+---------+---------+---------+---------+---------+ 2880
         ATGGTCGTTCGACATTACGCCCGTTCGTTCCCCGCGACCGTAACAGTCACGGTTGGCGGG
    2881 ---------+---------+---------+---------+---------+---------+ 2940
         CTAACGCCCGCGCCCGGGGAGGTGAGCGGTGAGGGACCTCCACGACTTTTTCCTGGCCCG
    2941 ---------+---------+---------+---------+---------+---------+ 3000
         GGTGGACGAACTGGTGCCGGAACTCCTACCCGGGGCGCGGCGGGTGGGCGACGAGTGGCG
    3001 ---------+---------+---------+---------+---------+---------+ 3060
         GGCGGGCTCGGTCCAGGGCGAGCGGGGCGACAGCCTGGCCGTGGACCGCGGGAAGGGCTT
    3061 ---------+---------+---------+---------+---------+---------+ 3120
         CTGGATCGACCACAACCCCTCGGCCCCCGAGCCCCGGCAGGGAAACCTCCTCACGCTGAT
    3121 ---------+---------+---------+---------+---------+---------+ 3180
         CCAGGCGGCCAAGGGGCTCTCCCCCGAGGAGGCCCGGCGCTGGGCCCAGCAGTGGCTTGG
    3181 ---------+---------+---------+---------+---------+---------+ 3240
         CCTCTCCCCTTCGCCAAAGGTCAGGCGGACGAGGAGCTCAGGACCAAAGGTCTTGAGTAC
    3241 ---------+---------+---------+---------+---------+---------+ 3300
         TCAAGTGCGTGGGAGCTCGGGTGCTCCAGTCCCTGAGTCTTCAGGTTCCCAGGTACCTGA
    3301 ---------+---------+---------+---------+---------+---------+ 3360
         GGAGTCGGACCCCTTTGACAACCCCCGCTTCCGGGACCTCCTCACCCCCAGGGGCGAGGA
    3361 ---------+---------+---------+---------+---------+---------+ 3420
         CGAGGCCCCCTTGGCCCCCGGCCTCCGAGGAGGTGCTGCGGCGCATGGTGTCTAGGCTTCT
    3421 ---------+---------+---.---+---------+---------+---------+ 3480
         CCGCACCCCCGAGGCCGTGGCCTACCTGAAGGGGCGCGGTCTGGATGCCCGGGTGGTCCG
    3481 ---------+---------+---------+---------+---------+---------+ 3540
         CCGCTTCTACCTCGGCCTGGACGACACCGCGCGGGCCACCGCCGCCCTGGTCTACCCGGT
    3541 ---------+---------+---------+---------+---------+---------+ 3600
         GATAGGGCCGGACGGCTCCCCCGTTCGCCGCCACCTCTACTACGAGATCCCCGGCCTCAC
    3601 ---------+---------+---------+---------+---------+---------+ 3660
         CCAGGGCGCCCCGGGCAAGGGCTGGGGGAGGGGGAGGCCCACCAGCTACTGGGCCCTCCC
                                                                      3720
```

9/13

FIG. 7C

```
       CCCCTTCGAGGGCCCCTCCCCCCGCCGCAAGCTCTTCTTGTGCGAGGGGGCGAAGGATGC
3721   --------+---------+---------+---------+---------+---------+   3780
       CTGGGCCCTCTGGCTCCACCTCCACGCCCAGCCCTGGGCCCAGGACCTGGCGGTGGTGAC
3781   --------+---------+---------+---------+---------+---------+   3840
       CTCCACGCACGGCTCCGCCCTCCCCGAGGCCTGGAAAGACCCCCTGTTCTGGGCCCCTTG
3841   --------+---------+---------+---------+---------+---------+   3900
       GGAGGAGGTCTACCTGGGCCAGGACGCCGACTCCGCCGGCGAGGAGATGGCCCGGAAGGT
3901   --------+---------+---------+---------+---------+---------+   3960
       GGCGGAGGTGGCGAGGCGGCCCGTCCGCCGCGTCCGGGTCCCGGAGGGGATGGGGAAGGA
3961   --------+---------+---------+---------+---------+---------+   4020
       CTGGACGGACTACTTCCTGGCGGGGGGGCACCCCCGAGGGCTTGCGCCTCCTCCTGGAGGG
4021   --------+---------+---------+---------+---------+---------+   4000
       AGCGGAGGTCTGGGAAGAAGAAGTGGCTGGAGGTGGGGCCAGGATCCAGCTCCCGGACCC
4081   --------+---------+---------+---------+---------+---------+   4140
       CGTGGACATCCAGCGGGCCTTCGTGCGGGGCCACCTCTACGTCCCCGTGCGGGTCCTGGA
4141   --------+---------+---------+---------+---------+---------+   4200
       GAACCGGGGGGAAGAAGGGGCCCGCTACCGCACCGTGGTGGTCCGCTCCGACGGGGCCGT
4201   --------+---------+---------+---------+---------+---------+   4260
       CCTGGGCTGGGGCTACTTGCCGGCCCCGCCCGGCACCCCCTTGGAGGACCGGGTGCTGGC
4261   --------+---------+---------+---------+---------+---------+   4320
       CGTGGACGACGGCACCATCATCCGCAGGCCCCCGAAGGCGGCCGCCGGGACCTCGTGGAA
4321   --------+---------+---------+---------+---------+---------+   4380
       CGGGGAGGCCATCAACCGCTTCCTGGAAGCCCGGGCCCGGGGAGTGAGCGCCATGACCGT
4381   --------+---------+---------+---------+---------+---------+   4440
       GGCCCCCCGGGACCTGCCTGGGCTCATCGTCCGCCACCTCCGCCAGGTGATCCTCCCCAG
4441   --------+---------+---------+---------+---------+---------+   4500
       TGAGGACGGCTACCTCCTGGCCGCCTTAGGGGTCATGACCTCCTACGTGCAGAGCGTCTT
4501   --------+---------+---------+---------+---------+---------+   4560
       CGACGCCGTGCCCCTCTTCCTCGTGGTGGGCCCGCCGGGCTCGGGGAAGACGGAGTTCGC
4561   --------+---------+---------+---------+---------+---------+   4620
       CCGCCTCATGGCCGAGCTGGGGGGCCAACGGCGTGGTGATCACCGGCCAGACCTCCGCCGC
4621   --------+---------+---------+---------+---------+---------+   4680
       CACCGCCGCCCGGATCATCGACGAGACGGGGGGGGCTGGTGGCCTTCGACGACCTGGAGGA
4681   --------+---------+---------+---------+---------+---------+   4740
       GGTGCGCCAGCGGTCGGGGGAGCGCTGAGGCCTCCCAGCTGGAGCAGTTCCTCAAGGTGTC
4741   --------+---------+---------+---------+---------+---------+   4800
       CTACAAGAAGGAGACCGCGGTCAAGAGCTGGACGGACACCAAGGGGATGCGGGTCCTCAC
4801   --------+---------+---------+---------+---------+---------+   4860
       CCTCAACTTCTTCGGGGGTCAAGGTGATCACCAACACCCAGGGGACGGGGGACATCCTGGG
4861   --------+---------+---------+---------+---------+---------+   4920
       GAGCCGGATGCTGGTCATCCGCACCGCCCGCCTCCGGGACCTGGGCAGAGGGGAGGAGCG
4921   --------+---------+---------+---------+---------+---------+   4980
       CCGCCCCGAGGGGCTCTCCCCCCCAGGCCCTCCAAGAACTCCGGGACAACCTCTACATCT
4981   --------+---------+---------+---------+---------+---------+   5040
       GGGCCATGGAGAACGCGGCCAGCCTCCACGCCCCTGTACCGGGAGCGCTTCGCGGGCAAGG
5041   --------+---------+---------+---------+---------+---------+   5100
       GGGAGCGCCTGGACGAGATCGCCGCCCCCCTTGCGTACCATCGCCCACCACCTGGGGGACG
5101   --------+---------+---------+---------+---------+---------+   5160
       AGGAGCTGGCGGCCCGCCTGGAGGACGCCCTGCGCCGGCAGGAAGGGCGCCTGGAGGAGA
5161   --------+---------+---------+---------+---------+---------+   5220
       CCCTTTCCGATGCCGAGGTGGTGGGAGACCGCCCTCAAGGAGGCCATCCGCCAGGGCTACC
5221   --------+---------+---------+---------+---------+---------+   5280
       GGAGCCACGTGGCCCTGGTCCACGTGATCTTCCAGGCCCGGAAGATCTTCGGGGACGACT
5281   --------+---------+---------+---------+---------+---------+   5340
       GGGGCCGGGAGCGCACCGTGGACATCCCCCGGTGGCGGGACCCCAAGTGGGTGGGGCAGA
5341   --------+---------+---------+---------+---------+---------+   5400
       TCGCCAGCAACTACGGCTGGGCGGCCCCAGAAAGGCCCGTGAGGCCCCGGCTTTGGGACA
5401   --------+---------+---------+---------+---------+---------+   5460
       AGCAGTTCCGCATCATGCGCCTGGAGCCCACCTTCGTGGAGCGGGTGGTCAGGGGCTTCC
5461   --------+---------+---------+---------+---------+---------+   5520
       TCCAGGAGGGGATCCCCTTGGAGCCCCTGAAGCAACCCCTGGCTTCTGCCTGGACACCCC
                                                                   5580
```

FIG. 7D

```
       CTGCGCCGAGTGCGCCTACCTGCACTGGTGCGACCTCCGGCCTGACAAGGAAAAGTGGCT
5581   --------+---------+---------+---------+---------+---------+   5640
       GGAGCGCTACGGGGAGGCCAAGCTGGCCCAGAAAAGGCGGGAGCTGGAGGAGGAGTTTTT
5641   --------+---------+---------+---------+---------+---------+   5700
       GGCCCTGGTGGGGCCCCAAGATGGCCTTGGCCTCCAGGCTTCCGCCGAGGAGGAGGGAGA
5701   --------+---------+---------+---------+---------+---------+   5760
       CCGAGGTAAGCACCCAAGTACCCAAGTACCCAAGACCCTAAAGCCTCAGGTACCGGAGGA
5761   --------+---------+---------+---------+---------+---------+   5820
       CCTCGGGGACGGAGGACCTAAAACCCCAAGGGCGTGAAAGACTGAGGTGAGAGGGATGAT
5821   --------+---------+---------+---------+---------+---------+   5880
       CGTGGCTGTCACCGGCTTCAAGGGAGGGGTGGGGAAGACCACCACGGCGGTCCACCTGGC
5881   --------+---------+---------+---------+---------+---------+   5940
       CTGCTTCCTGGCCGAGCGGGGCCCCACCCTGCTGGTCGGACGGGGACCCCAACCGCTCCGC
5941   --------+---------+---------+---------+---------+---------+   6000
       CACGGGGTGGCACCGGAGGGGGAGGCCTCCCGGTGACCGTGGTGGACGAGCGGGTGGCGGC
6001   --------+---------+---------+---------+---------+---------+   6060
       CCGGTACGCCCGGGAGCACGCCCACGTGGTCATAGACACCCAGGCCCGCCCCACGGAAGA
6061   --------+---------+---------+---------+---------+---------+   6120
       GGACCTCCGGGCCCTCGCCAAGGGGGTGGACCTGCTGGTCCTGCCCACGTCCCCCGACGC
6121   --------+---------+---------+---------+---------+---------+   6180
       CCTGGCCCTGGAGGCCCTCCTGGCCACCCTGGAAGCCCTGCGGGGGGCGGAGGCCCGCTT
6181   --------+---------+---------+---------+---------+---------+   6240
       CCGGGTCCTCCTGACCATGGTGCCCCCGCCCCCGAGCCGGGACGGGGAGGAGGCCCGGGC
6241   --------+---------+---------+---------+---------+---------+   6300
       CCTCTTGGGGGCGGAGGGCGTTCCCCTCTTCACAGGCTGGGTGAGGCGGGCGGCAGCCTT
6301   --------+---------+---------+---------+---------+---------+   6360
       CCCCAAGGCCGCCCTCCTGGGGGTGCCTGTCTACCGGGTGCCCGACCCCAGGGCGAGGCT
6361   --------+---------+---------+---------+---------+---------+   6420
       GGCCTGGGGGGACTACGCGCGGGTGGGGGAAGAGCTCCTGAAGGAGGTGGGGGGATGAGC
6421   --------+---------+---------+---------+---------+---------+   6480
       AAGTTCGCCAGGCTCCTCAAAGAGGTCAAGGAGAAGGAGGAGGCCTCCGGGGGAGCGGCCT
6481   --------+---------+---------+---------+---------+---------+   6540
       CGGGGGAAGAGCCGGCGGGAGGACTACGTGGCCATGAAGGTCTACATCAGCAAAGAGCTT
6541   --------+---------+---------+---------+---------+---------+   6600
       CACCGGAGGCTGAAGCTGAAGGCCCTGGAGGAGGAGAAGGAGCTTTCGGAGCTGGTGGAA
6601   --------+---------+---------+---------+---------+---------+   6660
       GAGGCCCTGAGGAAGTTGCTGGTGTGACCTCCTCCCGCCTCGTAGAGCGTGAAAAGGAGG
6661   --------+---------+---------+---------+---------+---------+   6720
       TAAGACGATGGTCACCCTTAACAAATCGCCCCTAGAAGCCCTCTACGCGGGCCACTCCCC
6721   --------+---------+---------+---------+---------+---------+   6780
       CCAGGAGGCGGGCCGTCTCTTCGAAGCGCCTGGTCCGCAAGATATTGAAGGAACTCCACC
6781   --------+---------+---------+---------+---------+---------+   6840
       CCATCTGGAGCCAAGAGTTCGTGGATGTCGTCCCTTGGTCCGAGCACGCCACCCGCAAGG
6841   --------+---------+---------+---------+---------+---------+   6900
       GGCTCAGGGCCACGGACATCGGCCGTGGACCTGGTGGGCTACGGGAAGGACGACAAGGTCT
6901   --------+---------+---------+---------+---------+---------+   6960
       ACGCCATCCAGGTCAAGCTGTGGGATAAGCCCCTCTCTTGGAAGGACCTGGGGAGCTTCG
6961   --------+---------+---------+---------+---------+---------+   7020
       TGGGGGTGGTGAACCACCCCGAGTACGGCTTCGACCACGGGCTCATCGTGGCCCCAAGAG
7021   --------+---------+---------+---------+---------+---------+   7080
       GCGTGACCCAGGAGGCCGACCGCCAGCTCCAGGGCCTACCCATCACCATCCTGAGCGAAG
7081   --------+---------+---------+---------+---------+---------+   7140
       AGGCTCTCCTAGAAGACCTGGACCTGGAATCCCTCGTTCCAGACCGCCCCGAGGAAGCCC
7141   --------+---------+---------+---------+---------+---------+   7200
       GCAGGCGGGGGAAGAAGGCCCTCCGTAAGTACCAGCAAGAAGCCTTAGAGGAGGTGGCCA
7201   --------+---------+---------+---------+---------+---------+   7260
       AAGCCTTCTTAGAGAAGGGCCTGCCCCGGGGCAAGCTCATCATGCCCCCGGGCACGGGCA
7261   --------+---------+---------+---------+---------+---------+   7320
       AGACCCTGGTGGCCCTCAAGATCGCCGAAAAGGTGGCGGGGCCCCGGGGGGGAGGGTCCTCT
7321   --------+---------+---------+---------+---------+---------+   7380
       TCCTGGCGCCCTCCATCGCCCTCCTGGACCAGTCCCTCAGGGCCTGGGCGGCGGAGGCTT
       --------+---------+---------+---------+---------+---------+   7440
```

BEST AVAILABLE COPY

11/13

```
     CCTTGCCCTTGCGCCTCTTCGCCGTGGTCTCGGACACGGGCGTGGGCAAGACCTCGGAGG
                                                                              7500
7441 --------+---------+---------+---------+---------+---------+
     ACGACCTCTCCGCCCTCTCCCTCCTCTCCATCCCTCCTACCACCAAGCCTGAGGAGCTGG
                                                                              7560
7501 --------+---------+---------+---------+---------+---------+
     CCTCCGAGGGCCAAGACGGAGAGTCAGGAGGCCCTCACCGTGGTCTTCTCCACCTACCAGT
                                                                              7620
7561 --------+---------+---------+---------+---------+---------+
     CGGCGGAGGTCCTGGAGAGGGCCCAGAAGGAGCACGGGCTTCCCCCTTTTGACCTGATGA
                                                                              7680
7621 --------+---------+---------+---------+---------+---------+
     TCCTGGACGAAGCCCACCGCACAGCCACGGTGCGGGCGGGAGAAGAAAGCCCCTTCACCA
                                                                              7740
7681 --------+---------+---------+---------+---------+---------+
     AGGTGCACCACGACCACTACGTGAAGGCCCGCCACCGCCTCTACATGACGGCCACGCCCA
                                                                              7800
7741 --------+---------+---------+---------+---------+---------+
     GGATCTGGGAGGTGGAGGGGAATGGAGAGAGGGGCCAAGGGAAAAAGGCGGCGAAAAAGA
                                                                              7860
7801 --------+---------+---------+---------+---------+---------+
     AGGACCCTCAGAAAGAGGGTTCTCCTCCCCTTTTGGACCTCGGTGCCTCTCCTACGGAGG
                                                                              7920
7861 --------+---------+---------+---------+---------+---------+
     ACTCCACGGCCCCCGAAGGGGTGGAACTCCTGGTCTACTCCATGGACAACGAGGGGATCT
                                                                              7980
7921 --------+---------+---------+---------+---------+---------+
     ATGGCCCCACCCTCTACGAGTACACCTTCACCCGCGCCGTGAAGGAGGGCCACCTGAGCG
                                                                              8040
7981 --------+---------+---------+---------+---------+---------+
     ACTACAAGGTCATCGTCTTCTCCGTGGCGGAGGAAGCCCAAAAGGACCTGGCCTCCTACC
                                                                              8100
8041 --------+---------+---------+---------+---------+---------+
     TCCAGGGACCCGAGGCCCTCAAGGTGGAGGAGGCTCTGAAGGCCCTGGGCCTGTGGAAGG
                                                                              8160
8101 --------+---------+---------+---------+---------+---------+
     TCCTCCAGGGGGAGGTGCGGGACGAGGAGGGGAACCCGATGGGGGGGCCTCGACCTGCGGA
                                                                              8220
8161 --------+---------+---------+---------+---------+---------+
     GAGTCATCGCCTTCCACGGCCGGGTGAAGGAGTCCAAGGAGATGGAGGAAGAGTTCACGA
                                                                              8280
8221 --------+---------+---------+---------+---------+---------+
     AGGTGGCCCTCGCTGCCCAGCAGGCTGGCCTCCTTCCCGAGGAGCTCCGGCGGGTGGAGG
                                                                              8340
8281 --------+---------+---------+---------+---------+---------+
     TGAAGCACATAGACGGGCAGATGTCCGCCTATGACCGGAAGCGCCTCCTGGACTGGCTTA
                                                                              8400
8341 --------+---------+---------+---------+---------+---------+
     GGGAGAACGTCCCCGAGGGGGGAGGTCCGCCTCCTCACCAACGCCAAGGTCCTCACCGAGG
                                                                              8460
8401 --------+---------+---------+---------+---------+---------+
     GGATCGACGTCCCCGGCCCTAGATGCCGTGGCCTTCATGCGTCCCCGGGACAGCGTGGTGG
                                                                              8520
8461 --------+---------+---------+---------+---------+---------+
     ACGTGATCCAGGCCGTGGGGGCGGGGCCATGCGCAAGGCCCCGGGCAAGGAGTACGGGTACG
                                                                              8580
8521 --------+---------+---------+---------+---------+---------+
     TGGTCCTGCCCGTGGTGGTGAGGGGGGCAGGACGAGGAGCGGGAGATCGAGGAGAGCGGCT
                                                                              8640
8581 --------+---------+---------+---------+---------+---------+
     ACCGGGCGGTGTGGCAGGTGCTCTCGGCCTTGCGCTCGGTGGACAAGTCCTTCGAGGCCC
                                                                              8700
8641 --------+---------+---------+---------+---------+---------+
     GCATGCGGGCCGCCCTGGTGCGCCTCTCGGGTAAGGGCGAGGGCGGGGAAGGTGGAGAGG
                                                                              8760
8701 --------+---------+---------+---------+---------+---------+
     CCCGAGAGGGTGTGGCCGTCATCGGGGAAGGAAGCGCCTCCCCCGTGATCGTAGATGTCC
                                                                              8820
8761 --------+---------+---------+---------+---------+---------+
     TTCAGGGGAACCTCAACCTCCACCAGGAGATCACCCGGAGCCTCGCCGGCAAGCTGGTCA
                                                                              8880
8821 --------+---------+---------+---------+---------+---------+
     GGCGCCTCGCCCTGGGGCGGAAGTACCTGGAGAACTGGGCCCAGGACGTGGCCCGGGTGG
                                                                              8940
8881 --------+---------+---------+---------+---------+---------+
     CGAAGGTGCTGGAGCAGCAGGTCAGGGCGATGGCGGAGCGGGACCCCAAGGTGAAGGAAA
                                                                              9000
8941 --------+---------+---------+---------+---------+---------+
     AACTGGGGAAACTCCTCGCCGCCCTGCAGGCCTTCACCAGCGAGAGCGTGACGGAGGACG
                                                                              9060
9001 --------+---------+---------+---------+---------+---------+
     AAGCCATCCTCATGCTGGTCCAGCACGCTCTCACCAAGCCCATCTTCGACGCCCTCTTCG
                                                                              9120
9061 --------+---------+---------+---------+---------+---------+
     GGGAACTCCTAGAAAAGCGGGAGGACCCCGTTTCCCGGGCCCTAGACGAACTCTTCCAGG
                                                                              9180
9121 --------+---------+---------+---------+---------+---------+
     AGTTCAGGGGGGTTCCTGGACCGGGAAGGGGGAGGCCCTCAAGGATTTCTACGAAGAGATGC
                                                                              9240
9181 --------+---------+---------+---------+---------+---------+
     GCCTCAAGGCCCTAGGGCTCACGGACGAAGCCGAAAGGGCCGACTTCCTACGGAGGCTCT
                                                                              9300
```

FIG. 7E

12/13

```
           ACTCCAACTTCTTCGCCCGGGCCTTCCCCCAGGTGGCCGACCAGGTGGGGATCGCCTACA
      9301 ---------+---------+---------+---------+---------+---------+    9360
           CCCCGGTGGAGCTGGTGGACTTCCTGGTGAAGAGCGCAGACGAGCTGGCCAGGAAGCACT
FIG. 7F   9361 ---------+---------+---------+---------+---------+---------+    9420
           GTTGGCCGGGGGCTCGATGGGGAGAAGGTCTTCATCCTGGAGCCCTTCGCCGGCACAGGC
      9421 ---------+---------+---------+---------+---------+---------+    9480
           ACCTTCGTCACCCGAATCCTGCACCGGGTAGCCGAAAGGGGCGGGGCCGACGCGGTCAAG
      9481 ---------+---------+---------+---------+---------+---------+    9540
           GGCAAGCTGGAGCGGGGGGGAGATCTGGGCCAACGAGATCCTTCTCCTCCCCTACTACGTC
      9541 ---------+---------+---------+---------+---------+---------+    9600
           CTCAGGGCCAACGTGGAGAACACCACCCTGGCCCTGACCGGGGAGTACGTCCCCTTCAAG
      9601 ---------+---------+---------+---------+ ----+---------+    9660
           GGGGCGTTCTGGCGGACTCCTTCGGCTGGCGGAGCTGGGGTATAGCGAGAAAAAGTTTGG
      9661 ---------+---------+---------+---------+---------+---------+    9720
           CATCATCCCGCTCTTCCCGGAAGAATACGGTGAGGCCCTGAACGAGCAGCTGAAGGCCCC
      9721 ---------+---------+---------+---------+---------+---------+    9780
           TATCCAGGTTATCCTCTCCAACCCCCCGTGCGGGCTTGGTTGGAGAAGGAGGGCGAGGGG
      9781 ---------+---------+---------+---------+---------+---------+    9840
           AAGAAGAACCCCGTCTACCGTAAGGTGCGGGGAGCGGGTGGAGCCAACCTATGTACGGCGG
      9841 ---------+---------+---------+---------+---------+---------+    9900
           GCCAAGGAACTTCCCATCGGGGGGGACAAAACCCAAGGGAGAGAACCTGAACTCCCTCTAC
      9901 ---------+---------+---------+---------+---------+---------+    9960
           GACCAGTACATCCAGGCCTTGCGGGTGGCGAGCGACCGTATCGGGGAGGAGGGGGTCGTG
      9961 ---------+---------+---------+---------+---------+---------+    10020
           GCCTTCGTCACCAACAACGGGTGGCTGGGGGGGCGTAGTGCCCCGGGGGCTTGCGGGCCTCT
      10021 ---------+---------+---------+---------+---------+---------+    10080
           TTGGCGGAGGAGTTCGCCGAGGTGTACGTCTACGACCTGAGGGGGGGATGCGAGGGAGAAG
      10081 ---------+---------+---------+---------+---------+---------+    10140
           GGGGAGGCACGGAAGAAGGAGGGGGGCGGGGTCTTTGGACAGCCTTCCCGCGCCGGGGTC
      10141 ---------+---------+---------+---------+---------+---------+    10200
           TGCCTCCTCCTCCTGGTGAAGCGTAAGGACCACAAAGGGATCGGCAAGGTCCACCTCTAT
      10201 ---------+---------+---------+---------+---------+---------+    10260
           CGGGTCGGGGACGGCCTCTCCCGGGAGGCCAAGCTGGCTCTGGTGAAGGAGCATGGCTCA
      10261 ---------+---------+---------+---------+---------+---------+    10320
           GTCTCTGGGTTCCCTGGCAAGAGGTTCCCTATGAAGAGTGGGTGGGGAGGCTTACCCCCG
      10321 ---------+---------+---------+---------+---------+---------+    10380
           GGTTCTCGGGGATGTTGTCCCTGGACGAGGTCTTTGAGGTGCGGAGTTCTGGGGTGAAGA
      10381 ---------+---------+---------+---------+---------+---------+    10440
           CCAACCGCGATGCCTACGTCTTCAACCCCTCCCGGGCGGAGCTGGAGCGGCACATGAGGC
      10441 ---------+---------+---------+---------+---------+---------+    10500
           GGCTCATCTCCACCTACAACGAGCACGTGAAAAGGAAAAAAGAGGGGAAACTAGGGGAAC
      10501 ---------+---------+---------+---------+---------+---------+    10560
           TGGAAAAGGATGAGAGCATCATCAAGTGGGATAGGGAACTCATCAGGTACCTAGAGTCCC
      10561 ---------+---------+---------+---------+---------+---------+    10620
           TGAGGGAAGCTTCCTACGAAGGGAGCGGTCAAGTCTACGAGGCCCTCTACCGCCCCTTCG
      10621 ---------+---------+----------+---------+---------+---------+    10680
           TGCCTATGTACCTCTACCTCAGCCGCACTTTCAATAGCATGATTTACCAAATCCCCCGCA
      10681 ---------+---------+---------+---------+---------+---------+    10740
           TCTGGCCCACCCCCGAGGCCGAGAACCTGGCCATCGCCGTGGCCGGAAAGGGGAGTAACG
      10741 ---------+---------+---------+---------+---------+---------+    10800
           CTTTTAGCGCTGTGGCCACCAGGAGGGTGGTTGACCTGCACTTTATTGAGACCACCCAGC
      10801 ---------+---------+---------+---------+---------+---------+    10860
           TCTACCCCCTTTACCACTACCCCGAAAACAGCCCTCTGGGGGGGACACCCAAAGCGCAAGC
      10861 ---------+---------+---------+---------+---------+---------+    10920
           TCAACCTCAAGGAGGAGTTCTTGAGGAAGCTTGGGGAGGTCCTCGGCCGCGCCCCGTTCCCC
      10921 ---------+---------+---------+---------+---------+---------+    10980
           CCGAGGAGGCCTTCGCTTACATCTACGCCGTGGTGAGCCACCCCCTCTACGCCGAGCGCT
      10981 ---------+---------+---------+---------+---------+---------+    11040
           TCGCCAAGGACCTCAAGATGGACCTCCCCCGCATTCCCCTCCCCCAAGATCCCGAACTCT
      11041 ---------+---------+---------+---------+---------+---------+    11100
           TTGCCAGGCTGGTGAAGGCGGGTCAAGAACTCATTCACCTCCACACCGAGTACGAGACCC
                 ---------+    11160
```

13/13

FIG. 7G

```
            TGCCCCCCTGGAGCCCAGTCCCCCTTCGGGTGGAAGAGGGAGGCCCGGAGGACCCTACGA
11161       ---------+---------+---------+---------+---------+---------+    11220
            GCGCTACCGGGTGGAGCGGATGAGGCTGGACAAGGAGAGGAGGGTTCTCCAGTACAACGA
11221       ---------+---------+---------+---------+---------+---------+    11280
            CTGGGTCCGGGTGGAGGGCATCCCCGAGGAGGCCTTCCGCTGGCGCCCCGGGGGGTACTC
11281       ---------+---------+---------+---------+---------+---------+    11340
            CCCCTTGGAGTGGATTGGCCGCTTCTGGAAGGTGGAGGAGAAGGTGCCCAAGGGCAGGGG
11341       ---------+---------+---------+---------+---------+---------+    11400
            GGAGGCCATCGTCTGGGACCCCAACCTCTTCCTCAAGGAGAAGGGGGAACCCCGTTACCT
11401       ---------+---------+---------+---------+---------+---------+    11460
            CCTGGACCTCATCGGGCGGGCGGTCCAGGTGGCCGTGCAGACGGTTGGGATCCACGAGGA
11461       .--------+---------+---------+---------+---------+---------+    11520
            GCTGAGAGAAGACGTGGAAGCTCTGCTGGGTTGAGGGGGTGCTGGCCCGCCGTTCTCCCT
11521       ---------+---------+---------+---------+---------+---------+    11580
            ACTCCTTTAGGGCCTACCCCTACGATCCAAGCACGGCCCTGGGGGGCGCTCAGGTGGGCA
11581       ---------+---------+---------+---------+---------+---------+    11640
            TCCCACGTCCAAGGCCCCGACTTGGGCACCCCATGCTGCGAACTTACAGCCCAAGGGCCT
11641       ---------+---------+---------+---------+---------+---------+    11700
            GAAACATTCCCCCCTGCTCACGGGGGGAAAGTTCGTGAAGGAAAGAGCAAAGCCTTTTTTA
11701       ---------+---------+---------+---------+---------+---------+    11760
            TCGCATCCGGAGAGATGGCGGGGTGGAACTTTTCCCCGAGGACTCCCCCATAGGGACATG
11761       ---------+---------+---------+---------+---------+---------+    11820
            TAAACGGCAAGCTATCAGTGTAGACTTTTTTCAAAAAGAGCCATACTCGTGTTTTCCCGT
11821       ---------+---------+---------+---------+---------+---------+    11880
            TCAGAACGGCATTTTTGCTAAGGAGGTGGTTTACAAATGGGTGTTAATGCGCTACATCCT
11881       ---------+---------+---------+---------+---------+---------+    11940
            CCGGTAGTAGGAGCATGC
11941       ---------+--------  11958
```